

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number:

10/807,517A

Source:

FW/6

Date Processed by STIC:

7/13/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 07/13/2006

PATENT APPLICATION: US/10/807,517A

TIME: 08:43:40

Input Set : F:\P-2762-US3.txt

Output Set: N:\CRF4\07132006\J807517A.raw

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3 <110> APPLICANT: GTx, Inc.
4     et al., Steiner
5     Steiner, Et al.,
7 <120> TITLE OF INVENTION: ISOLATED NUCLEIC ACIDS ENCODING RAT P-HYDE PROTEIN
9 <130> FILE REFERENCE: P-2762-US3
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/807,517A
C--> 11 <141> CURRENT FILING DATE: 2004-03-24
11 <160> NUMBER OF SEQ ID NOS: 11
13 <170> SOFTWARE: PatentIn version 3.3
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 1886
17 <212> TYPE: DNA
18 <213> ORGANISM: Human
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25 cccgatgagg ccccaaaagt gagcatcctg ggtagcgggg actttgcccg ctccctggcc      180
27 acacgcctgg tgggctctgg cttaaagtgt gtggtgggga gccgcaacce caaacgcaca      240
29 gccaggtgtt tccctcagc ggcccaagtgt actttccaag aggaggcagt gagctccccg      300
31 gaggtcatct ttgtggctgt gttccgggag cactactctt cactgtgcag tctcagtgc      360
33 cagctggcgg gcaagatcct ggtggatgtg agcaacccta cagagcaaga gcaccttcag      420
35 catcgtgagt ccaatgctga gtacctggcc tccctcttcc ccacttgcac agtggccaag      480
37 gccttcaatg tcactctctg ctggacctgt caggctggcc caagggatgg taacgggcag      540
39 gtgcccactt gcggtgacca gccagaagcc aagcgtgctg tctcggagat ggcgctcgcc      600
41 atgggcttca tgcccggtga catgggatac ctggcgtagc cctgggaggt ggaggccatg      660
43 cccctgcgcc tccctccggc ctggaagggtg cccaccctgc tggccctggg gctcttcgtc      720
45 tgcttctatg cctacaactt cgtccgggac gttctgcagc cctatgtgca ggaaagccag      780
47 aacaagttct tcaagctgcc cgtgtccgtg gtcaacacca cactgccgtg cgtggcctac      840
49 gtgctgctgt cactcgtgta cttgcccggc gtgctggcgg ctgccctgca gctgcggcgc      900
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53 atcgggctgc tcagcttctt ctgcgcgcgc ctgcacgccc tctacagctt ctgcttgccg      1020
55 ctgcgcgcgc cccaccgcta cgacctggtc aacctggcag tcaagcaggt cttggccaac      1080
57 aagagccacc tctgggtgga ggaggtctgg cggatggaga tctacctctc cctgggagtg      1140
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61 ctcaactgga gggagttcag cttcgttcag tcctcactgg gctttgtggc cctcgtgctg      1260
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75 aggtttgagg tccaaattcc tgggactcaa atgtatgcag tactattcag aatgatatac      1680
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98          20          25          30
101 Ile Leu Gly Ser Gly Asp Phe Ala Arg Ser Leu Ala Thr Arg Leu Val
102          35          40          45
105 Gly Ser Gly Phe Lys Val Val Val Gly Ser Arg Asn Pro Lys Arg Thr
106          50          55          60
109 Ala Arg Leu Phe Pro Ser Ala Ala Gln Val Thr Phe Gln Glu Glu Ala
110 65          70          75          80
113 Val Ser Ser Pro Glu Val Ile Phe Val Ala Val Phe Arg Glu His Tyr
114          85          90          95
117 Ser Ser Leu Cys Ser Leu Ser Asp Gln Leu Ala Gly Lys Ile Leu Val
118          100         105         110
121 Asp Val Ser Asn Pro Thr Glu Gln Glu His Leu Gln His Arg Glu Ser
122          115         120         125
125 Asn Ala Glu Tyr Leu Ala Ser Leu Phe Pro Thr Cys Thr Val Val Lys
126          130         135         140
129 Ala Phe Asn Val Ile Ser Ala Trp Thr Leu Gln Ala Gly Pro Arg Asp
130 145         150         155         160
133 Gly Asn Gly Gln Val Pro Ile Cys Gly Asp Gln Pro Glu Ala Lys Arg
134          165         170         175
137 Ala Val Ser Glu Met Ala Leu Ala Met Gly Phe Met Pro Val Asp Met
138          180         185         190
141 Gly Ser Leu Ala Ser Ala Trp Glu Val Glu Ala Met Pro Leu Arg Leu
142          195         200         205
145 Leu Pro Ala Trp Lys Val Pro Thr Leu Leu Ala Leu Gly Leu Phe Val
146          210         215         220
149 Cys Phe Tyr Ala Tyr Asn Phe Val Arg Asp Val Leu Gln Pro Tyr Val
150 225         230         235         240
153 Gln Glu Ser Gln Asn Lys Phe Phe Lys Leu Pro Val Ser Val Val Asn
154          245         250         255
157 Thr Thr Leu Pro Cys Val Ala Tyr Val Leu Leu Ser Leu Val Tyr Leu
158          260         265         270
161 Pro Gly Val Leu Ala Ala Ala Leu Gln Leu Arg Arg Gly Thr Lys Tyr
162          275         280         285
165 Gln Arg Phe Pro Asp Trp Leu Asp His Trp Leu Gln His Arg Lys Gln
166          290         295         300
169 Ile Gly Leu Leu Ser Phe Cys Ala Ala Leu His Ala Leu Tyr Ser
170 305         310         315         320
173 Phe Cys Leu Pro Leu Arg Arg Ala His Arg Tyr Asp Leu Val Asn Leu

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177 Ala Val Lys Gln Val Leu Ala Asn Lys Ser His Leu Trp Val Glu Glu
178          340          345          350
181 Val Trp Arg Met Glu Ile Tyr Leu Ser Leu Gly Val Leu Ala Leu Gly
182          355          360          365
185 Thr Leu Ser Leu Leu Ala Val Thr Ser Leu Pro Ser Ile Ala Asn Ser
186          370          375          380
189 Leu Asn Trp Arg Glu Phe Ser Phe Val Gln Ser Ser Leu Gly Phe Val
190 385          390          395          400
193 Ala Leu Val Leu Ser Thr Leu His Thr Leu Thr Tyr Gly Trp Thr Arg
194          405          410          415
197 Ala Phe Glu Glu Ser Arg Tyr Lys Phe Tyr Leu Pro Pro Thr Phe Thr
198          420          425          430
201 Leu Thr Leu Leu Val Pro Cys Val Val Ile Leu Ala Lys Ala Leu Phe
202          435          440          445
205 Leu Leu Pro Cys Ile Ser Arg Arg Leu Ala Arg Ile Arg Arg Gly Trp
206          450          455          460
209 Glu Arg Glu Ser Thr Ile Lys Phe Thr Leu Pro Thr Asp His Ala Leu
210 465          470          475          480
213 Ala Glu Lys Thr Ser His Val
214          485
217 <210> SEQ ID NO: 3
218 <211> LENGTH: 2118
219 <212> TYPE: DNA
220 <213> ORGANISM: Human
222 <400> SEQUENCE: 3
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225 atggacaagc cactgatcag cctccacctg gtggacagcg atagtagcct tgccaaggctc 120
227 cccgatgagg ccccaaaagt gagcatcctg ggtagcgggg actttgcccg ctccctggcc 180
229 acacgcctgg tgggctctgg cttcaaagtg gtggtgggga gccgcaacc caaacgcaca 240
231 gccaggctgt ttccctcagc ggcccaagtg actttccaag aggaggcagt gagctccccg 300
233 gaggtcatct ttgtggctgt gttccgggag cactactctt cactgtgcag tctcagtgac 360
235 cagctggcgg gcaagatcct ggtggatgtg agcaacccta cagagcaaga gcaccttcag 420
237 catcgtgagt ccaatgctga gtacctggcc tccctcttcc ccacttgac agtggtcaag 480
239 gccttcaatg tcatctctgc ctggacctg caggetggcc caagggatgg taacgggcag 540
241 gtgcccattc gcggtgacca gccagaagcc aagcgtgctg tctcggagat ggcgctcgcc 600
243 atgggcttca tgcccggtga catgggatcc ctggcgctcag cctgggaggt ggaggccatg 660
245 cccctgcgcc tctcccgcc ctggaagggt cccacctgc tggccctggg gctcttcgtc 720
247 tgcttctatg cctacaactt cgtccgggac gttctgcagc cctatgtgca ggaaagccag 780
249 aacaagttct tcaagctgcc cgtgtccgtg gtcaacacca cactgccgtg cgtggcctac 840
251 gtgctgctgt cactcgtgta cttgcccggc gtgctggcgg ctgccctgca gctgcggcgc 900
253 ggcaccaagt accagcgctt ccccgactgg ctggaccact ggctacagca ccgcaagcag 960
255 atcgggctgc tcagcttctt ctgcgcgcc ctgcacgccc tctacagctt ctgcttgccg 1020
257 ctgcgcgcgc cccaccgcta cgacctggtc aacctggcag tcaagcaggt cttggccaac 1080
259 aagagccacc tctgggtgga ggaggtctgg cggatggaga tctacctctc cctgggagtg 1140
261 ctggccctcg gcacgttgct cctgctggcc gtgacctcac tgccgtccat tgcaaactcg 1200
263 ctcaactgga gggagttcag cttcgttcag tgtgtggcaa cttccagtgc aggaacaca 1260
265 ggcagtggaa cccgaagacc tgaatctcag tcccaagacc ccacttacc tgccccgcac 1320
267 catcagacaa gtttcttagg cctcgggagc ttctgctgct cacttgctgcc tgtgtccacc 1380

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271 cagtggcatg ctggcttttg agtcctcact gggctttgtg gccctcgtgc tgagcacact 1500
273 gcacacgctc acctacggct ggacccgcgc cttcgaggag agccgctaca agttctacct 1560
275 gcctcccacc ttcacgtca cgtgctggt gccctgcgtc gtcctcctgg ccaaagccct 1620
277 gtttctcctg ccctgcatca gccgcagact cgccaggatc cggagaggct gggagaggga 1680
279 gagcaccatc aagttcacgc tgcccacaga ccacgccctg gccgagaaga cgagccacgt 1740
281 atgaggtgcc tgccctgggc tctggacccc gggcacacga gggacggtgc cctgagcccc 1800
283 ttaggttttc ttttcttggt ggtgcaaagt ggtataactg tgtgcaaata ggaggtttga 1860
285 ggtccaaatt cctgggactc aaatgtatgc agtactattc agaatgatat acacacatat 1920
287 gtgtatatgt atttaccata attccacata tataacagga tttgcaatta tacatagcta 1980
289 gctaaaaagt tgggtctctg agatttcaac ttgtagattt aaaaacaagt gccgtacgtt 2040
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299 <213> ORGANISM: Human
301 <400> SEQUENCE: 4
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311 Ile Leu Gly Ser Gly Asp Phe Ala Arg Ser Leu Ala Thr Arg Leu Val
312 35 40 45
315 Gly Ser Gly Phe Lys Val Val Val Gly Ser Arg Asn Pro Lys Arg Thr
316 50 55 60
319 Ala Arg Leu Phe Pro Ser Ala Ala Gln Val Thr Phe Gln Glu Glu Ala
320 65 70 75 80
323 Val Ser Ser Pro Glu Val Ile Phe Val Ala Val Phe Arg Glu His Tyr
324 85 90 95
327 Ser Ser Leu Cys Ser Leu Ser Asp Gln Leu Ala Gly Lys Ile Leu Val
328 100 105 110
331 Asp Val Ser Asn Pro Thr Glu Gln Glu His Leu Gln His Arg Glu Ser
332 115 120 125
335 Asn Ala Glu Tyr Leu Ala Ser Leu Phe Pro Thr Cys Thr Val Val Lys
336 130 135 140
339 Ala Phe Asn Val Ile Ser Ala Trp Thr Leu Gln Ala Gly Pro Arg Asp
340 145 150 155 160
343 Gly Asn Gly Gln Val Pro Ile Cys Gly Asp Gln Pro Glu Ala Lys Arg
344 165 170 175
347 Ala Val Ser Glu Met Ala Leu Ala Met Gly Phe Met Pro Val Asp Met
348 180 185 190
351 Gly Ser Leu Ala Ser Ala Trp Glu Val Glu Ala Met Pro Leu Arg Leu
352 195 200 205
355 Leu Pro Ala Trp Lys Val Pro Thr Leu Leu Ala Leu Gly Leu Phe Val
356 210 215 220
359 Cys Phe Tyr Ala Tyr Asn Phe Val Arg Asp Val Leu Gln Pro Tyr Val
360 225 230 235 240
363 Gln Glu Ser Gln Asn Lys Phe Phe Lys Leu Pro Val Ser Val Val Asn

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364          245          250          255
367 Thr Thr Leu Pro Cys Val Ala Tyr Val Leu Leu Ser Leu Val Tyr Leu
368          260          265          270
371 Pro Gly Val Leu Ala Ala Ala Leu Gln Leu Arg Arg Gly Thr Lys Tyr
372          275          280          285
375 Gln Arg Phe Pro Asp Trp Leu Asp His Trp Leu Gln His Arg Lys Gln
376          290          295          300
379 Ile Gly Leu Leu Ser Phe Phe Cys Ala Ala Leu His Ala Leu Tyr Ser
380 305          310          315          320
383 Phe Cys Leu Pro Leu Arg Arg Ala His Arg Tyr Asp Leu Val Asn Leu
384          325          330          335
387 Ala Val Lys Gln Val Leu Ala Asn Lys Ser His Leu Trp Val Glu Glu
388          340          345          350
391 Val Trp Arg Met Glu Ile Tyr Leu Ser Leu Gly Val Leu Ala Leu Gly
392          355          360          365
395 Thr Leu Ser Leu Leu Ala Val Thr Ser Leu Pro Ser Ile Ala Asn Ser
396          370          375          380
399 Leu Asn Trp Arg Glu Phe Ser Phe Val Gln Cys Val Ala Thr Ser Ser
400 385          390          395          400
403 Ala Gly Asn Thr Gly Ser Gly Thr Arg Arg Pro Glu Ser Gln Ser Gln
404          405          410          415
407 Asp Pro His Leu Pro Ala Pro His His Gln Thr Ser Phe Leu Gly Pro
408          420          425          430
411 Arg Ser Phe Cys Cys Ser Leu Val Pro Val Ser Thr Pro Tyr Gly His
412          435          440          445
415 Gln Glu Asp Leu Ser Trp Thr Arg
416          450          455

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419 <210> SEQ ID NO: 5

420 <211> LENGTH: 2714

421 <212> TYPE: DNA

422 <213> ORGANISM: Rat

424 <400> SEQUENCE: 5

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429 agtgggcatc ctgggcagcg gggattttgc ccggtccctg gccacacgcc tggtagggctc      180
431 tggcttcttt gtggtggtgg gaagccgtaa ccccaaacgc actgccggcc tcttccctc      240
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439 cgagtacctg gcctccctct tccctgcctg cactgtgggtc aaggccttca acgtcatctc      480
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/13/2006
PATENT APPLICATION: US/10/807,517A TIME: 08:43:41

Input Set : F:\P-2762-US3.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:10,11

VERIFICATION SUMMARY

DATE: 07/13/2006

PATENT APPLICATION: US/10/807,517A

TIME: 08:43:41

Input Set : F:\P-2762-US3.txt

Output Set: N:\CRF4\07132006\J807517A.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date